

This amendment is made without prejudice and are not to be construed as abandonment of the previously claimed subject matter or agreement with the Examiner's position. In accordance with the requirements of 37 C.F.R. § 1.121, a marked up version showing the changes to the claims, is attached herewith as Appendix A. For the Examiner's convenience, a complete claim set of the currently pending claims is also submitted herewith as Appendix B.

### **REMARKS**

#### **Status of the Claims.**

Claims 26-28, and 47-50 are pending with entry of this amendment, claims 37-38 being canceled and claims 47-50 being added herein. Claim 26 is amended herein. This amendment introduces no new matter. Claim 26 is amended to eliminate reference to SEQ ID NO:10 and to eliminate the hybridization language. New claims 47-50 are drawn to the method previously recited in claim 26 using SEQ ID NO:10.

#### **Discrepancy in Claim Numbering.**

The Examiner noted a discrepancy in claim numbering. In particular, the Examiner alleged that claims referred to as claims 36 and 37 in the response filed on May 8, 2002 should be designated as claims 37 and 38 respectively. Consistent with the Examiner's position and the Office Action of July 01, 2001, Applicants herein after refer to these claims as claims 37 and 38.

#### **35 U.S.C. §102.**

The rejection of claims 26-28 and 37 under 35 U.S.C. §102(a) as allegedly anticipated by Tanner *et al.* (1995) *Clin. Cancer Res.*, 1: 1455-1461 or Tanner *et al.* (1996) 56: 3441-3445 was maintained. In particular, the Examiner alleged that a nucleic acid consisting essentially of SEQ ID NO:9 would hybridize to the RMC20C001 probe disclosed by Tanner *et al.*

Applicants have amended claim 26 in accordance with the Examiner's recommendation to eliminate the hybridization language. Accordingly, claim 26, and dependent claims 27 and 28 are not anticipated by the cited references and the rejection of these claims under 35 U.S.C. §102(a) should be withdrawn.

New claims 47-50 are directed to the method utilizing:

[A] probe that hybridizes selectively to a target polynucleotide sequence **consisting essentially of the sequence of SEQ. ID. No. 10.**

The method of claims 47-50 **does not** persist in reading on a method utilizing a polypeptide comprising SEQ ID NO:9. Moreover, as shown in Figure 3, there is no overlap between RMC20C001 of Tanner *et al.* and the nucleic acid of SEQ ID NO:10. Accordingly, claims 47-50 are not anticipated by either of the cited references.

In view of this amendment, Applicants respectfully request that the rejections under 35 U.S.C. §102(a) be withdrawn.

**Obviousness-type double patenting.**

Claims 26-28, 36 and 37 were rejected under the judicially created doctrine of obviousness-type double patenting allegedly being unpatentable over claims 24-26, 35-36, and 38 of copending Application No: 08/731,499. Claims 26-28, 36 and 37 were rejected under the judicially created doctrine of obviousness-type double patenting allegedly being unpatentable over claims 26-28, 37-38, 56-57, and 61-63 of copending Application No: 08/785,532. Upon an indication of otherwise allowable subject matter, Applicants will provide a Terminal Disclaimer thereby obviating this rejection.

**Form of claims 37 and 38.**


Claims 37 and 38 were objected to under 37 C.F.R. §1.75© as allegedly being of improper dependent form for failing to further limit the subject matter of a previous claim (claim 26). Claims 37 and 38 are cancelled with entry of this amendment thereby obviating this rejection.

In view of the foregoing, Applicants believes all claims now pending in this application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If a telephone conference would expedite prosecution of this application, the Examiner is invited to telephone the undersigned at (510) 337-7871.

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Respectfully submitted,



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APPENDIX A

"MARKED UP" CLAIMS ILLUSTRATING THE AMENDMENTS MADE TO THE  
CLAIMS OF 08/892,695 WITH ENTRY OF THIS AMENDMENT

26. A method of screening for neoplastic cells in a sample, the method comprising:

contacting a nucleic acid sample from a human patient with a probe [~~which hybridizes selectively to a target polynucleotide sequence~~] consisting essentially of a sequence [~~selected from the group consisting~~] of SEQ. ID. No. 9, [~~and SEQ. ID. No. 10,~~] wherein the probe is contacted with the sample under conditions in which the probe specifically hybridizes under stringent conditions with the target polynucleotide sequence to form a stable hybridization complex; and

detecting the formation of a hybridization complex, wherein an amplification of said target polynucleotide sequence indicates that said cell is a neoplastic cell.

--47. (New) A method of screening for neoplastic cells in a sample, the method comprising:

contacting a nucleic acid sample from a human patient with a probe that hybridizes selectively to a target polynucleotide sequence consisting essentially of the sequence of SEQ. ID. No. 10, wherein the probe is contacted with the sample under conditions in which the probe specifically hybridizes under stringent conditions with the target polynucleotide sequence to form a stable hybridization complex; and

detecting the formation of a hybridization complex, wherein an amplification of said target polynucleotide sequence indicates that said cell is a neoplastic cell.

48. (New) The method of claim 47, wherein the nucleic acid sample is from a patient with breast cancer.

49. (New) The method of claim 47, wherein the nucleic acid sample is a metaphase spread or an interphase nucleus.

50. (New) The method of claim 47, wherein the probe comprises a polynucleotide sequence as set forth in SEQ. ID. No. 10.--